Figure 1

Recombinant murine met OB (double stranded) DNA and amino acid sequence (SEQ. ID. NOs.: 1, 2, and 3).

```
     TCTAGATTTGAGTTTTAACTTTTAGAAGGAGGAATAACATATGGTACCGATCCAGAAAGT
  9 -+---------+---------+---------+---------+---------+-------- 68
     AGATCTAAACTCAAAATTGAAAATCTTCCTCCTTATTGTATACCATGGCTAGGTCTTTCA
                                              M  V  P  I  Q  K  V  -

     TCAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCA
 69 -+---------+---------+---------+---------+---------+-------- 128
     AGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT
      Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I  N  D  I  S  H  -

     CACCCAGTCGGTCTCCGCTAAACAGCGTGTTACCGGTCTGGACTTCATCCCGGGTCTGCA
129 -+---------+---------+---------+---------+---------+-------- 188
     GTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGACCTGAAGTAGGGCCCAGACGT
      T  Q  S  V  S  A  K  Q  R  V  T  G  L  D  F  I  P  G  L  H  -

     CCCGATCCTAAGCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGGTGTTAAC
189 -+---------+---------+---------+---------+---------+-------- 248
     GGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCCACAATTG
      P  I  L  S  L  S  K  M  D  Q  T  L  A  V  Y  Q  Q  V  L  T  -

     CTCCCTGCCGTCCCAGAACGTTCTTCAGATCGCTAACGACCTCGAGAACCTTCGCGACCT
249 -+---------+---------+---------+---------+---------+-------- 308
     GAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCTGGAGCTCTTGGAAGCGCTGGA
      S  L  P  S  Q  N  V  L  Q  I  A  N  D  L  E  N  L  R  D  L  -

     GCTGCACCTGCTGGCATTCTCCAAATCCTGCTCCCTGCCGCAGACCTCAGGTCTTCAGAA
309 -+---------+---------+---------+---------+---------+-------- 368
     CGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGGCGTCTGGAGTCCAGAAGTCTT
      L  H  L  L  A  F  S  K  S  C  S  L  P  Q  T  S  G  L  Q  K  -

     ACCGGAATCCCTGGACGGGGTCCTGGAAGCATCCCTGTACAGCACCGAAGTTGTTGCTCT
369 -+---------+---------+---------+---------+---------+-------- 428
     TGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACATGTCGTGGCTTCAACAACGAGA
      P  E  S  L  D  G  V  L  E  A  S  L  Y  S  T  E  V  V  A  L  -

     GTCCCGTCTGCAGGGTTCCCTTCAGGACATCCTTCAGCAGCTGGACGTTTCTCCGGAATG
429 -+---------+---------+---------+---------+---------+-------- 488
     CAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGTCGACCTGCAAAGAGGCCTTAC
      S  R  L  Q  G  S  L  Q  D  I  L  Q  Q  L  D  V  S  P  E  C  -

     TTAATGGATCC
489 -+---------
     AATTACCTAGG
```

Figure 2

Recombinant human met OB analog (Double Stranded) DNA and amino acid sequence (SEQ. ID. NOs.: 4, 5 and 6).

```
     CATATGGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTAATTAAAACGATCGTT
   1 ---------+---------+---------+---------+---------+---------+ 60
     GTATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAA

        M  V  P  I  Q  K  V  Q  D  D  T  K  T  L  I  K  T  I  V  -

     ACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAACAGCGTGTTACAGGC
  61 ---------+---------+---------+---------+---------+---------+ 120
     TGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCG

     T  R  I  N  D  I  S  H  T  Q  S  V  S  S  K  Q  R  V  T  G  -

     CTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAAATGGACCAGACCCTG
 121 ---------+---------+---------+---------+---------+---------+ 180
     GACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGAC

     L  D  F  I  P  G  L  H  P  I  L  T  L  S  K  M  D  Q  T  L  -

     GCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTTCTTCAGATCTCTAAC
 181 ---------+---------+---------+---------+---------+---------+ 240
     CGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTG

     A  V  Y  Q  Q  I  L  T  S  M  P  S  R  N  V  L  Q  I  S  N  -

     GACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTG
 241 ---------+---------+---------+---------+---------+---------+ 300
     CTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGAC

     D  L  E  N  L  R  D  L  L  H  V  L  A  F  S  K  S  C  H  L  -

     CCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGT
 301 ---------+---------+---------+---------+---------+---------+ 360
     GGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCA

     P  W  A  S  G  L  E  T  L  D  S  L  G  G  V  L  E  A  S  G  -

     TACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGG
 361 ---------+---------+---------+---------+---------+---------+ 420
     ATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACC

     Y  S  T  E  V  V  A  L  S  R  L  Q  G  S  L  Q  D  M  L  W  -

     CAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC
 421 ---------+---------+---------+---- 454
     GTCGACCTGGACAGAGGCCCAACAATTACCTAGG

     Q  L  D  L  S  P  G  C  *
```

Figure 3A

Recombinant human metFc-OB (double stranded) DNA) and amino acid sequence (SEQ. ID. NOs.: 7, 8 and 9).

```
      CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA
   1  ---------+---------+---------+---------+---------+---------+ 60
      GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT

        M  E  P  K  S  C  D  K  T  H  T  C  P  P  C  P  A  P  E   -

      CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
  61  ---------+---------+---------+---------+---------+---------+ 120
      GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG

      L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D  T  L  M  I   -

      TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
 121  ---------+---------+---------+---------+---------+---------+ 180
      AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG

      S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D  P  E  V   -

      AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG
 181  ---------+---------+---------+---------+---------+---------+ 240
      TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC

      K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  T  K  P  R  E   -

      GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG
 241  ---------+---------+---------+---------+---------+---------+ 300
      CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC

      E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W   -

      CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
 301  ---------+---------+---------+---------+---------+---------+ 360
      GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC

      L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P  A  P  I  E   -

      AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA
 361  ---------+---------+---------+---------+---------+---------+ 420
      TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT

      K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P   -

      TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
 421  ---------+---------+---------+---------+---------+---------+ 480
      AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA

      S  R  D  E  L  T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y   -

      CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
 481  ---------+---------+---------+---------+---------+---------+ 540
      GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG
```

Figure 3B

```
      P  S  D  I  A  V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T   -

      ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC
 541  ---------+---------+---------+---------+---------+---------+ 600
      TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG

      T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D   -

      AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC
 601  ---------+---------+---------+---------+---------+---------+ 660
      TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG

      K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H   -

      AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT
 661  ---------+---------+---------+---------+---------+---------+ 720
      TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA

      N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  V  P  I  Q  K  V   -

      CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC
 721  ---------+---------+---------+---------+---------+---------+ 780
      GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG

      Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I  N  D  I  S  H   -

      ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC
 781  ---------+---------+---------+---------+---------+---------+ 840
      TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG

      T  Q  S  V  S  S  K  Q  K  V  T  G  L  D  F  I  P  G  L  H   -

      CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC
 841  ---------+---------+---------+---------+---------+---------+ 900
      GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG

      P  I  L  T  L  S  K  M  D  Q  T  L  A  V  Y  Q  Q  I  L  T   -

      TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG
 901  ---------+---------+---------+---------+---------+---------+ 960
      AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC

      S  M  P  S  R  N  V  I  Q  I  S  N  D  L  E  N  L  R  D  L   -

      CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT
 961  ---------+---------+---------+---------+---------+---------+ 1020
      GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA

      L  H  V  L  A  F  S  K  S  C  H  L  P  W  A  S  G  L  E  T   -

      CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG
1021  ---------+---------+---------+---------+---------+---------+ 1080
      GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC

      L  D  S  L  G  G  V  L  E  A  S  G  Y  S  T  E  V  V  A  L   -
```

Figur 3C

```
     TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT
1081 ---------+---------+---------+---------+---------+---------+ 1140
     AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA

     S  R  L  Q  G  S  L  Q  D  M  L  W  Q  L  D  L  S  P  G  C   -

     TAATGGATCC
1141 ---------+ 1150
     ATTACCTAGG

     *         -
```

Figure 4A

Recombinant human metFc-OB (double stranded) DNA and amino acid sequence (SEQ. ID. NOs.: 10, 11 and 12).

```
      CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA
    1 ---------+---------+---------+---------+---------+---------+ 60
      GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT

          M  E  P  K  S  A  D  K  T  H  T  C  P  P  C  P  A  P  E   -

      CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
   61 ---------+---------+---------+---------+---------+---------+ 120
      GAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG

       L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D  T  L  M  I   -

      TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
  121 ---------+---------+---------+---------+---------+---------+ 180
      AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG

       S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D  P  E  V   -

      AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG
  181 ---------+---------+---------+---------+---------+---------+ 240
      TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC

       K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  T  K  P  R  E   -

      GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG
  241 ---------+---------+---------+---------+---------+---------+ 300
      CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC

       E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W   -

      CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
  301 ---------+---------+---------+---------+---------+---------+ 360
      GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC

       L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P  A  P  I  E   -

      AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA
  361 ---------+---------+---------+---------+---------+---------+ 420
      TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT

       K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P   -

      TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
  421 ---------+---------+---------+---------+---------+---------+ 480
      AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA

       S  R  D  E  L  T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y   -

      CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
  481 ---------+---------+---------+---------+---------+---------+ 540
      GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG
```

Figure 4B

```
     P  S  D  I  A  V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  -

     ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC
 541 ---------+---------+---------+---------+---------+---------+ 600
     TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG

     T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  -

     AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC
 601 ---------+---------+---------+---------+---------+---------+ 660
     TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG

     K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  -

     AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT
 661 ---------+---------+---------+---------+---------+---------+ 720
     TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA

     N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  V  P  I  Q  K  V  -

     CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC
 721 ---------+---------+---------+---------+---------+---------+ 780
     GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG

     Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I  N  D  I  S  H  -

     ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC
 781 ---------+---------+---------+---------+---------+---------+ 840
     TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG

     T  Q  S  V  S  S  K  Q  K  V  T  G  L  D  F  I  P  G  L  H  -

     CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC
 841 ---------+---------+---------+---------+---------+---------+ 900
     GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG

     P  I  L  T  L  S  K  M  D  Q  T  L  A  V  Y  Q  Q  I  L  T  -

     TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG
 901 ---------+---------+---------+---------+---------+---------+ 960
     AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC

     S  M  P  S  R  N  V  I  Q  I  S  N  D  L  E  N  L  R  D  L  -

     CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT
 961 ---------+---------+---------+---------+---------+---------+ 1020
     GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA

     L  H  V  L  A  F  S  K  S  C  H  L  P  W  A  S  G  L  E  T  -

     CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG
1021 ---------+---------+---------+---------+---------+---------+ 1080
     GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC

     L  D  S  L  G  G  V  L  E  A  S  G  Y  S  T  E  V  V  A  L  -
```

Figure 4C

```
     TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT
1081 ---------+---------+---------+---------+---------+---------+ 1140
     AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA

     S  R  L  Q  G  S  L  Q  D  M  L  W  Q  L  D  L  S  P  G  C   -

     TAATGGATCC
1141 ---------+ 1150
     ATTACCTAGG

     *  -
```

Figure 5A

Recombinant human metFc-OB (double stranded) DNA and amino acid sequence (SEQ. ID. NOs.: 13, 14 and 15).

```
     CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT
   1 ---------+---------+---------+---------+---------+---------+ 60
     GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA

         M  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P   -

     TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
  61 ---------+---------+---------+---------+---------+---------+ 120
     AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

      S  V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E   -

     GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 121 ---------+---------+---------+---------+---------+---------+ 180
     CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

      V  T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y   -

     GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 181 ---------+---------+---------+---------+---------+---------+ 240
     CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

      V  D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S   -

     ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
 241 ---------+---------+---------+---------+---------+---------+ 300
     TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

      T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E   -

     TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
 301 ---------+---------+---------+---------+---------+---------+ 360
     ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

      Y  K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K   -

     GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 361 ---------+---------+---------+---------+---------+---------+ 420
     CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

      A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L   -

     ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 421 ---------+---------+---------+---------+---------+---------+ 480
     TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

      T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A   -

     GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
 481 ---------+---------+---------+---------+---------+---------+ 540
     CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
```

Figure 5B

```
      V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L   -

     GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 541 ---------+---------+---------+---------+---------+---------+ 600
     CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

      D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q   -

     CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
 601 ---------+---------+---------+---------+---------+---------+ 660
     GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q   -

     AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA
 661 ---------+---------+---------+---------+---------+---------+ 720
     TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT

      K  S  L  S  L  S  P  G  K  V  P  I  Q  K  V  Q  D  D  T  K   -

     ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC
 721 ---------+---------+---------+---------+---------+---------+ 780
     TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG

      T  L  I  K  T  I  V  T  R  I  N  D  I  S  H  T  Q  S  V  S   -

     TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG
 781 ---------+---------+---------+---------+---------+---------+ 840
     AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC

      S  K  Q  K  V  T  G  L  D  F  I  P  G  L  H  P  I  L  T  L   -

     TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT
 841 ---------+---------+---------+---------+---------+---------+ 900
     AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA

      S  K  M  D  Q  T  L  A  V  Y  Q  Q  I  L  T  S  M  P  S  R   -

     AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA
 901 ---------+---------+---------+---------+---------+---------+ 960
     TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT

      N  V  I  Q  I  S  N  D  L  E  N  L  R  D  L  L  H  V  L  A   -

     TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC
 961 ---------+---------+---------+---------+---------+---------+ 1020
     AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG

      F  S  K  S  C  H  L  P  W  A  S  G  L  E  T  L  D  S  L  G   -

     GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT
1021 ---------+---------+---------+---------+---------+---------+ 1080
     CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA

      G  V  L  E  A  S  G  Y  S  T  E  V  V  A  L  S  R  L  Q  G   -
```

Figur 5C

```
     TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC
1081 ---------+---------+---------+---------+---------+----- 1135
     AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG

     S  L  Q  D  M  L  W  Q  L  D  L  S  P  G  C  *     -
```

Figure 6A

Recombinant human metFc-OB (double stranded) DNA and amino acid sequence (SEQ. ID. NOs.: 16, 17 and 18).

```
     CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG
   1 ---------+---------+---------+---------+---------+---------+ 60
     GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC

         M  D  K  T  H  T  C  P  P  C  P  A  P  E  L  E  G  G  P  -

     TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
  61 ---------+---------+---------+---------+---------+---------+ 120
     AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

      S  V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  -

     GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 121 ---------+---------+---------+---------+---------+---------+ 180
     CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

      V  T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  -

     GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 181 ---------+---------+---------+---------+---------+---------+ 240
     CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

      V  D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  -

     ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT
 241 ---------+---------+---------+---------+---------+---------+ 300
     TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA

      T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  A  -

     TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
 301 ---------+---------+---------+---------+---------+---------+ 360
     ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

      Y  A  C  A  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  -

     GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 361 ---------+---------+---------+---------+---------+---------+ 420
     CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

      A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  -

     ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 421 ---------+---------+---------+---------+---------+---------+ 480
     TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

      T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  -

     GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
 481 ---------+---------+---------+---------+---------+---------+ 540
     CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
```

Figure 6B

```
     V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L   -

     GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 541 ---------+---------+---------+---------+---------+---------+ 600
     CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

     D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q   -

     CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
 601 ---------+---------+---------+---------+---------+---------+ 660
     GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

     Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q   -

     AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA
 661 ---------+---------+---------+---------+---------+---------+ 720
     TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT

     K  S  L  S  L  S  P  G  K  V  P  I  Q  K  V  Q  D  D  T  K   -

     ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC
 721 ---------+---------+---------+---------+---------+---------+ 780
     TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG

     T  L  I  K  T  I  V  T  R  I  N  D  I  S  H  T  Q  S  V  S   -

     TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG
 781 ---------+---------+---------+---------+---------+---------+ 840
     AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC

     S  K  Q  K  V  T  G  L  D  F  I  P  G  L  H  P  I  L  T  L   -

     TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT
 841 ---------+---------+---------+---------+---------+---------+ 900
     AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA

     S  K  M  D  Q  T  L  A  V  Y  Q  Q  I  L  T  S  M  P  S  R   -

     AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA
 901 ---------+---------+---------+---------+---------+---------+ 960
     TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT

     N  V  I  Q  I  S  N  D  L  E  N  L  R  D  L  L  H  V  L  A   -

     TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC
 961 ---------+---------+---------+---------+---------+---------+ 1020
     AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG

     F  S  K  S  C  H  L  P  W  A  S  G  L  E  T  L  D  S  L  G   -

     GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT
1021 ---------+---------+---------+---------+---------+---------+ 1080
     CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA

     G  V  L  E  A  S  G  Y  S  T  E  V  V  A  L  S  R  L  Q  G   -
```

Figure 6C

```
     TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC
1081 ---------+---------+---------+---------+---------+----- 1135
     AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG

     S  L  Q  D  M  L  W  Q  L  D  L  S  P  G  C  *       -
```